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ABSTRACT

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A general neural network based method and system for identifying peptide binding motifs from limited experimental data. In particular, an artificial neural network (ANN) is trained with peptides with known sequence and function (*i.e.*, binding strength) identified from a phage display library. The ANN is then challenged with unknown peptides, and predicts relative binding motifs. Analysis of the unknown peptides validate the predictive capability of the ANN.

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